Ebola virus surveillance in pigs presenting for slaughter in Uganda

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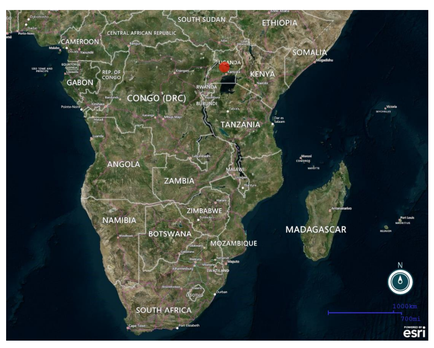
Introduction

Why Uganda?

Uganda has experienced five Ebola outbreaks with human index cases unable to account for their source of infection.[1] Additionally, in the past 30 years the pig population in Uganda has increased by more than tenfold to meet growing consumer demand for pork. Recent media coverage has raised doubts on the safety of pork in urban markets (see below).




Daily Monitor

Most pork in Kampala is unsafe - health experts

50 per cent

Why pigs?

In 2008, *Reston Ebolavirus* was isolated from domestic pigs during a disease investigation in the Philippines.[2] Five people in contact with the sick pigs, also tested positive for antibodies to Reston Ebolavirus, indicating likely transmission from pigs to humans.[2]

Subsequent to this, domestic pigs were experimentally infected with Zaire Ebolavirus confirming that they could shed the virus and infect other animals, under laboratory conditions.[3,4]

In addition to *Ebolavirus*, pigs have also been associated with several emerging zoonotic diseases including *Hepatitis E virus*,[5] *Nipah virus*,[6] *Ndumu virus*,[7] *Menangle virus*,[8] *swine influenza virus*[9] and *Bungowannah virus*.[10]

Objectives

- Determine if pigs in Uganda are infected with emerging and endemic zoonotic diseases – *Ebolavirus, Henipaviruses, Hepatitis E virus, Leptospira spp., Coxiella burnetii* and *Brucella spp.*
    1. At what levels?
    2. What are the risk factors for infection in pigs?
- Map pig trading routes, volumes and practices to identify possible surveillance and intervention points

Methods

We performed repeated cross-sectional sampling of pigs presenting for slaughter during months when previous human Ebola outbreaks occurred in the country and over holiday periods when pork consumption increases. Wambizzi abattoir is the only registered pig slaughterhouse in Uganda and is a catchment location for pigs from many districts surrounding Kampala, the capital. This makes it ideal for collection of a large variety of samples, from a large geographic area. At least 157 pigs must be sampled at each of the four time periods, for a total of 628 pigs assuming:

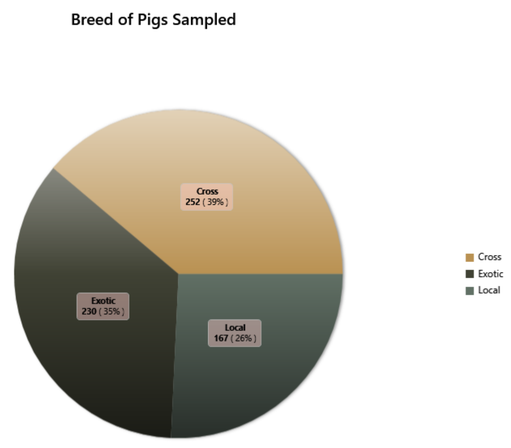
- *Ebolavirus* prevalence of at least 2%
- Diagnostic sensitivity of 95%
- Diagnostic specificity of 100% and
- Confidence level of 95%

Secondly, to determine effective locations for implementation of future surveillance and mitigation measures, pig trader network analysis to map pig trade volumes and routes is being done in conjunction with slaughterhouse surveillance.

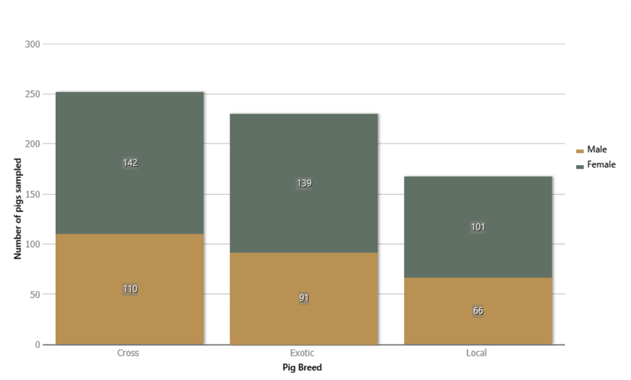
Results

A total of 6,600 samples were collected from 667 pigs sampled between December 2015 and October 2016. . Ten (10) samples were taken from each pig (blood, sera, feces, nasal swab, lung, liver, kidney, spleen, tracheobronchial lymph node, and uterus or epididymis) and collection of a nasopharyngeal flush from pigs with a temperature of 40^0 C or greater at time of slaughter. All samples were stored in duplicate.

Biodata was collected from 658 (98.6%) of the 667 sampled pigs. Seven percent of pigs (n=46) had a fever (>39.8^0 C) at the time of sampling, indicating active infection at the time.



Based on visual inspection, 35% of pigs sampled were exotic breeds, or improved breeds such as Landrace and Large White. Thirty-nine percent were crossbreeds and the remaining 26% were local breeds, characterized by small body size and poor growth characteristics.



Females made up 59% of the sampled pigs.

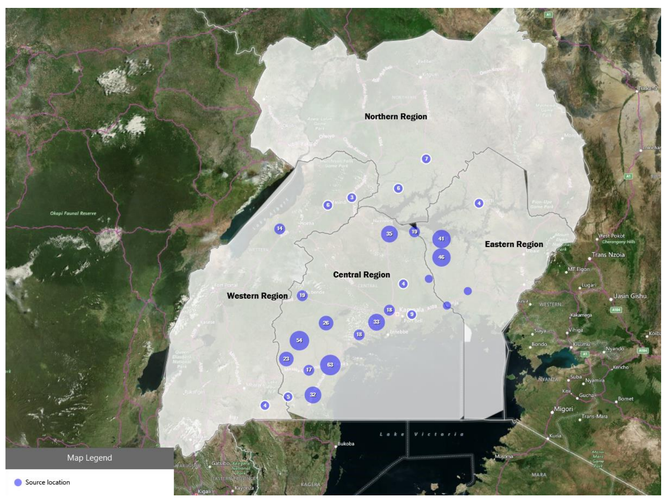


Image: Source Location of pigs sampled

Source location was collected for 76.4% of pigs sampled (n=510) to at least district level. 71% (n=360) of pigs were from the Central region, followed by 22% (n=112) from the Eastern region, 5% (n=24) from the Western region and the remaining 3% (n=14) from the North.

Coxiella burnetii, pathogenic *Leptospira spp.*, *Brucella abortus* and *Brucella melintensis* were detected by real-time PCR. All other laboratory analysis is ongoing.

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